

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,796A
Source: PCP/10
Date Processed by STIC: 5/19/05

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,796A

DATE: 05/19/2005
TIME: 10:15:53

Input Set : A:\Seqlist.txt
Output Set: N:\CRF4\05182005\J511796A.raw

4 <110> APPLICANT: Sode, Koji
 6 <120> TITLE OF INVENTION: GLUCOSE DEHYDROGENASE BETA-SUBUNIT AND
 7 DNA ENCODING THE SAME
 9 <130> FILE REFERENCE: TOYA126.002APC
 11 <140> CURRENT APPLICATION NUMBER: 10/511,796A
 12 <141> CURRENT FILING DATE: 2004-10-19
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/05375
 15 <151> PRIOR FILING DATE: 2003-04-25
 17 <150> PRIOR APPLICATION NUMBER: JP 2002-125353
 18 <151> PRIOR FILING DATE: 2002-04-26
 20 <160> NUMBER OF SEQ ID NOS: 19
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2467
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Burkholderia cepacia
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (258) ... (761)
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (764) ... (2380)
 W--> 36 <221> CDS
 37 <222> LOCATION: (2386) ... (2466)
 W--> 39 <400> 1
 40 aagctttctg tttgattgca cgcgattcta accgagcgtc tgtgaggcgaa aacgcgacat 60
 41 gcttcgtgtc gcacacgtgt cgccgcgacg acacaataat gcagcgaaat ggctgatcgt 120
 42 tacgaatggc tgacacattt aatggactat aaaaccattt tccgttccgg aatgtgcgcg 180
 43 tacatttcag gtccgcgccc atttttggaa aatatcaaggc gtggttttcc cgaatccgg 240
 44 gttcgagaga aggaaac atg cac aac gac act ccc cac tcg cgt cgc 290
 45 Met His Asn Asp Asn Thr Pro His Ser Arg Arg
 46 1 5 10
 48 cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa 338
 49 His Gly Asp Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln
 50 15 20 25
 52 ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tcg ctg aca ttg 386
 53 Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu
 54 30 35 40
 56 cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg 434
 57 Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met
 58 45 50 55
 60 acg ctt tcc gaa tcg ctg acc ggc aag aaa ggg ctc agc cgc gtg atc 482
 61 Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile
 62 60 65 70 75

P. 6

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64 ggc gag cgc ctg ctg cag gcg ctc cag aag ggc tcg ttc aag acg gcc	530
65 Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala	
66 80 85 90	
68 gac agc ctg ccg cag ctc gcc ggc gcg ctc gct ggc tcc ggt tcg ctg acg	578
69 Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr	
70 95 100 105	
72 cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gac gcc tgg tat ctc	626
73 Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu	
74 110 115 120	
76 ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc	674
77 Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe	
78 125 130 135	
80 ggc gtc gtg tcc gat acg ctc gtg atc cgt tcg tat tgc ccc aac aaa	722
81 Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys	
82 140 145 150 155	
84 ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc	769
85 Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala	
86 160 165 170	
88 gat acc gat acg caa aag gcc gac gtc gtc gtt gga tcg ggt gtc	817
89 Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val	
90 175 180 185	
92 gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg	865
93 Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val	
94 190 195 200	
96 atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag	913
97 Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu	
98 205 210 215	
100 cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg	961
101 Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro	
102 220 225 230	
104 tcg agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac	1009
105 Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr	
106 235 240 245 250	
108 ctg atc ctg aag ggc gag cac aag ttc aac tcg cag tac atc cgc gcg	1057
109 Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile Arg Ala	
110 255 260 265	
112 gtg ggc ggc acg acg tgg cac tgg gcc gcg tcg gcg tgg cgc ttc att	1105
113 Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg Phe Ile	
114 270 275 280	
116 ccg aac gac ttc aag atg aag agc gtg tac ggc gtc ggc cgc gac tgg	1153
117 Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg Asp Trp	
118 285 290 295	
120 ccg atc cag tac gac gat ctc gag ccg tac tat cag cgc gcg gag gaa	1201
121 Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala Glu Glu	
122 300 305 310	
124 gag ctc ggc gtg tgg ggc ccg ggc ccc gag gaa gat ctg tac tcg ccg	1249
125 Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr Ser Pro	
126 315 320 325 330	
128 cgc aag cag ccg tat ccg atg ccg ccg ctg ccg ttg tcg ttc aac gag	1297

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129 Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe Asn Glu		
130 335 340 345		
132 cag acc atc aag acg gcg ctg aac aac tac gat ccg aag ttc cat gtc	1345	
133 Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe His Val		
134 350 355 360		
136 gtg acc gag ccg gtc gcg cgc aac agc cgc ccg tac gac ggc cgc ccg	1393	
137 Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly Arg Pro		
138 365 370 375		
140 act tgt tgc ggc aac aac aac tgc atg ccg atc tgc ccg atc ggc gcg	1441	
141 Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile Gly Ala		
142 380 385 390		
144 atg tac aac ggc atc gtg cac gtc gag aag gcc gaa cgc gcc ggc gcg	1489	
145 Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala Gly Ala		
146 395 400 405 410		
148 aag ctg atc gag aac gcg gtc tac aag ctc gag acg ggc ccg gac	1537	
149 Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp		
150 415 420 425		
152 aag cgc atc gtc gcg gcg ctc tac aag gac aag acg ggc gcc gag cat	1585	
153 Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala Glu His		
154 430 435 440		
156 cgc gtc gaa ggc aag tat ttc gtg ctc gcc gcg aac ggc atc gag acg	1633	
157 Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile Glu Thr		
158 445 450 455		
160 ccg aag atc ctg ctg atg tcc gcg aac cgc gat ttc ccg aac ggt gtc	1681	
161 Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn Gly Val		
162 460 465 470		
164 gcg aac agc tcg gac atg gtc ggc cgc aac ctg atg gac cat ccg ggc	1729	
165 Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly		
166 475 480 485 490		
168 acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc	1777	
169 Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly		
170 495 500 505		
172 ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc	1825	
173 Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg		
174 510 515 520		
176 gcg acc gaa gcg gcg aag aag atc cac ctg tcg aac ctg tcg cgc atc	1873	
177 Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile		
178 525 530 535		
180 gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc	1921	
181 Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro		
182 540 545 550		
184 gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag	1969	
185 Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln		
186 555 560 565 570		
188 ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg	2017	
189 Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val		
190 575 580 585		
192 ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc	2065	
193 Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile		

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194	590	595	600	
196	acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc			2113
197	Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			
198	605	610	615	
200	gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg			2161
201	Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val			
202	620	625	630	
204	tcc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tcg acg atc			2209
205	Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile			
206	635	640	645	650
208	atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg			2257
209	Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr			
210	655	660	665	
212	tcc gac cat ccg aac ctg ttc att tcg acg acg gcg atg ccg acc			2305
213	Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met Pro Thr			
214	670	675	680	
216	gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg			2353
217	Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			
218	685	690	695	
220	atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc			2403
221	Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu			
222	700	705	710	
224	act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg			2451
225	Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala			
226	715	720	725	
228	gcc gat gcg gcc gat c			2467
229	Ala Asp Ala Ala Asp			
230	730			
233	<210> SEQ ID NO: 2			
234	<211> LENGTH: 168			
235	<212> TYPE: PRT			
236	<213> ORGANISM: Burkholderia cepacia			
238	<400> SEQUENCE: 2			
239	Met His Asn Asp Asn Thr Pro His Ser Arg Arg His Gly Asp Ala Ala			
240	1	5	10	15
241	Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln Gly Ala Leu Ala Leu			
242	20	25	30	
243	Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp			
244	35	40	45	
245	Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser			
246	50	55	60	
247	Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu			
248	65	70	75	80
249	Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln			
250	85	90	95	
251	Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser			
252	100	105	110	
253	Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn			
254	115	120	125	

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255 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
256      130          135          140
257 Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala
258      145          150          155          160
259 Asp Lys Pro Ile Glu Arg Gln Ala
260          165
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 539
265 <212> TYPE: PRT
266 <213> ORGANISM: Burkholderia cepacia
268 <400> SEQUENCE: 3
269 Met Ala Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser
270 1          5          10          15
271 Gly Val Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys
272          20          25          30
273 Ala Val Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile
274          35          40          45
275 Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro
276          50          55          60
277 Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn
278 65          70          75          80
279 Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile
280          85          90          95
281 Arg Ala Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg
282          100         105         110
283 Phe Ile Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg
284          115         120         125
285 Asp Trp Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala
286          130         135         140
287 Glu Glu Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr
288 145          150          155          160
289 Ser Pro Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe
290          165         170         175
291 Asn Glu Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe
292          180         185         190
293 His Val Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly
294          195         200         205
295 Arg Pro Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile
296          210         215         220
297 Gly Ala Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala
298 225          230          235          240
299 Gly Ala Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly
300          245          250          255
301 Pro Asp Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala
302          260          265          270
303 Glu His Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile
304          275          280          285
305 Glu Thr Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn
306          290          295          300

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/19/2005
PATENT APPLICATION: US/10/511,796A TIME: 10:15:54

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 6,17,18,19,22

Seq#:17; Xaa Pos. 2,3

VERIFICATION SUMMARY

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L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:413 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
M:341 Repeated in SeqNo=10
L:846 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0